

# SEQUENCE LISTING

<110> Hoxie, James A.  
Lin, George

<120> Compositions, Methods and Kits Relating to Deletion Mutations of  
Immunodeficiency Virus gp120 Hypervariable Regions

<130> 053893-5046

<150> 60/443,364

<151> 2003-01-29

<160> 30

<170> PatentIn version 3.2

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<212> DNA

<213> HIV-2/VCP (env)

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 <213> HIV-2/VCP (gp120)  
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 Pro Ala Trp Arg Asn Ala Ser Ile Pro Leu Phe Cys Ala Thr Lys Asn  
 35 40 45  
 Arg Asp Thr Trp Gly Thr Ile Gln Cys Leu Pro Asp Asn Asp Asp Tyr

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Thr Val Thr Glu Gln Ala Val Glu Asp Val Trp Asn Leu Phe Glu Thr 85 90 95		
Ser Ile Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Ala Met Asn 100 105 110		
Cys Thr Arg Asn Met Thr Thr Ser Thr Gly Thr Thr Asp Thr Gln Asn 115 120 125		
Ile Thr Ile Ile Asn Asp Thr Ser Pro Cys Val Arg Ala Asp Asn Cys 130 135 140		
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Gly Leu Glu Arg Asp Lys Arg Lys Gln Tyr Thr Glu Ala Trp Tyr Ser 165 170 175		
Lys Asp Val Ile Cys Asp Asn Asn Thr Ser Ser Arg Ser Lys Cys Tyr 180 185 190		
Met Asn His Cys Asn Thr Ser Val Ile Thr Glu Ser Cys Asp Lys His 195 200 205		
Tyr Trp Asp Ala Met Arg Phe Arg Tyr Cys Ala Pro Pro Gly Phe Ala 210 215 220		
Leu Leu Arg Cys Asn Asp Thr Asn Tyr Ser Gly Phe Ala Pro Asn Cys 225 230 235 240		
Ser Lys Val Val Ala Ala Thr Cys Thr Arg Met Met Glu Thr Gln Ser 245 250 255		
Ser Thr Trp Phe Gly Phe Asn Gly Thr Arg Ala Glu Asn Arg Thr Tyr 260 265 270		
Ile Tyr Trp His Gly Lys Asn Asn Arg Thr Ile Ile Ser Leu Asn Asn 275 280 285		

Phe Tyr Asn Leu Thr Met His Cys Lys Arg Pro Gly Asn Lys Thr Val  
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Leu Pro Ile Met Ser Gly Phe Lys Phe His Ser Lys Pro Val Ile Asn  
305 310 315 320

Lys Lys Pro Arg Gln Ala Trp Cys Trp Phe Lys Gly Glu Trp Lys Glu  
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Ala Met Gln Glu Val Lys Glu Thr Leu Ala Lys His Pro Arg Tyr Lys  
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Gly Asn Arg Ser Arg Thr Glu Asn Ile Lys Phe Lys Ala Pro Gly Arg  
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Gly Ser Asp Pro Glu Ala Ala Tyr Met Trp Thr Asn Cys Arg Gly Glu  
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Phe Leu Tyr Cys Asn Met Thr Trp Phe Leu Asn Trp Val Asp Asn Arg  
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Thr Gly Gln Lys Gln Arg Asn Tyr Ala Pro Cys His Ile Arg Gln Ile  
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Ile Asn Thr Trp His Arg Val Gly Lys Asn Val Tyr Leu Pro Pro Arg  
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Glu Gly Glu Leu Thr Cys Asn Ser Thr Val Thr Ser Ile Ile Ala Asn  
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Ile Asp Thr Gly Asp Gln Thr Asp Ile Thr Phe Ser Ala Glu Val Ala  
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Glu Leu Tyr Arg Leu Glu Leu Gly Asp Tyr Lys Leu Val Glu Ile Thr  
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Pro Ile Gly Phe Ala Pro Thr Ser Val Lys Arg Tyr Ser Ser Ala His  
485 490 495

Gln Arg His Thr Arg Gly Val Phe Val Leu Gly Phe Leu Gly Phe Leu  
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Ala Thr Ala Gly Ser Ala Met Gly Ala Ala Ser Leu Thr Leu Thr Ala  
515 520 525

Gln Ser Arg Thr Ser Leu Ala Gly Ile Val Gln Gln Gln Gln Gln Leu  
530 535 540

Leu Asp Val Val Lys Lys Gln Gln Glu Met Leu Arg Leu Thr Val Trp  
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Gly Thr Lys Asn Leu Gln Ala Arg Val Thr Ala Ile Glu Lys Tyr Leu  
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Cys His Thr Ser Val Pro Trp Val Asn Asp Ser Leu Thr Pro Asp Trp  
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Asn Asn Met Thr Trp Gln Glu Trp Glu Gln Lys Val Arg Tyr Trp Glu  
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Ala Asn Ile Ser Gln Ser Leu Glu Gln Ala Gln Ile Gln Gln Glu Lys  
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Asn Leu Tyr Glu Leu Gln Lys Leu Asn Ser Trp Gly Val Phe Thr Asn  
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Trp Leu Asp Phe Thr Ser Trp Val Arg Tyr Ile Gln Tyr Gly Val Tyr  
660 665 670

Val Val Val Gly Ile Val Ala Leu Arg Ile Val Ile Tyr Ile Val Gln  
675 680 685

Met Leu Ser Arg Leu Arg Lys Gly Tyr Arg Pro Val Phe Ser Ser Pro  
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Pro Gly Tyr Ile Gln Gln Ile His Ile His Lys Asp Gln Glu Gln Pro  
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Ser Trp Leu

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Pro Ala Trp Arg Asn Ala Ser Ile Pro Leu Phe Cys Ala Thr Lys Asn  
35 40 45

Arg Asp Thr Trp Gly Thr Ile Gln Cys Leu Pro Asp Asn Asp Asp Tyr  
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Gln Glu Ile Ala Leu Asn Val Thr Glu Ala Phe Asp Ala Trp Asn Asn  
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Thr Val Thr Glu Gln Ala Val Glu Asp Val Trp Asn Leu Phe Glu Thr  
85 90 95

Ser Ile Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Ala Met Asn  
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Cys Thr Arg Asn Met Thr Thr Ser Thr Gly Thr Thr Asp Thr Gln Asn  
115 120 125

Ile Thr Ile Ile Asn Asp Thr Ser Pro Cys Val Arg Ala Asp Asn Cys  
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Thr Gly Leu Lys Glu Glu Glu Met Val Asp Cys Gln Phe Asn Met Thr  
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Gly Leu Glu Arg Asp Lys Arg Lys Gln Tyr Thr Glu Ala Trp Tyr Ser  
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Lys Asp Val Ile Cys Asp Asn Asn Thr Ser Ser Arg Ser Lys Cys Tyr  
180 185 190



Met Asn His Cys Asn Thr Ser Val Ile Thr Glu Ser Cys Asp Lys His  
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Tyr Trp Asp Ala Met Arg Phe Arg Tyr Cys Ala Pro Pro Gly Phe Ala  
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Leu Leu Arg Cys Asn Asp Thr Asn Tyr Ser Gly Phe Ala Pro Asn Cys  
 225 230 235 240

Ser Lys Val Val Ala Ala Thr Cys Thr Arg Met Met Glu Thr Gln Ser  
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Ser Thr Trp Phe Gly Phe Asn Gly Thr Arg Ala Glu Asn Arg Thr Tyr  
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Ile Tyr Trp His Gly Lys Asn Asn Arg Thr Ile Ile Ser Leu Asn Asn  
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Phe Tyr Asn Leu Thr Met His Cys Lys Arg Pro Gly Asn Lys Thr Val  
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Leu Pro Ile Met Ser Gly Phe Lys Phe His Ser Lys Pro Val Ile Asn  
 305 310 315 320

Lys Lys Pro Arg Gln Ala Trp Cys Trp Phe Lys Gly Glu Trp Lys Glu  
 325 330 335

Ala Met Gln Glu Val Lys Glu Thr Leu Ala Lys His Pro Arg Tyr Lys  
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Gly Asn Arg Ser Arg Thr Glu Asn Ile Lys Phe Lys Ala Pro Gly Arg  
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Gly Ser Asp Pro Glu Ala Ala Tyr Met Trp Thr Asn Cys Arg Gly Glu  
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Phe Leu Tyr Cys Asn Met Thr Trp Phe Leu Asn Trp Val Asp Asn Arg  
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Thr Gly Gln Lys Gln Arg Asn Tyr Ala Pro Cys His Ile Arg Gln Ile  
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Ile Asn Thr Trp His Arg Val Gly Lys Asn Val Tyr Leu Pro Pro Arg  
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Glu Gly Glu Leu Thr Cys Asn Ser Thr Val Thr Ser Ile Ile Ala Asn  
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Ile Asp Thr Gly Asp Gln Thr Asp Ile Thr Phe Ser Ala Glu Val Ala  
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Glu Leu Tyr Arg Leu Glu Leu Gly Asp Tyr Lys Leu Val Glu Ile Thr  
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<213> HIV-2/VCP (gp41)

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Lys Gln Gln Glu Met Leu Arg Leu Thr Val Trp Gly Thr Lys Asn Leu  
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Gln Ala Arg Val Thr Ala Ile Glu Lys Tyr Leu Lys Asp Gln Ala Gln  
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Leu Asn Ser Trp Gly Cys Ala Phe Arg Gln Val Cys His Thr Ser Val  
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Pro Trp Val Asn Asp Ser Leu Thr Pro Asp Trp Asn Asn Met Thr Trp

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Gln Lys Leu Asn Ser Trp Gly Val Phe Thr Asn Trp Leu Asp Phe Thr		
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Ser Trp Val Arg Tyr Ile Gln Tyr Gly Val Tyr Val Val Val Gly Ile		
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Arg Lys Gly Tyr Arg Pro Val Phe Ser Ser Pro Pro Gly Tyr Ile Gln		
	195 200	205
Gln Ile His Ile His Lys Asp Gln Glu Gln Pro Ala Arg Glu Glu Thr		
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Glu Glu Asp Val Gly Ser Asn Gly Gly Asp Arg Ser Trp Leu Pro Ile		
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Ala Tyr Ile His Phe Leu Ile Arg Leu Leu Ile Arg Leu Leu Ile Gly		
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Leu Tyr Asn Ile Cys Arg Asp Leu Leu Ser Arg Ile Ser Pro Ile Leu		
	260 265	270
Gln Pro Ile Phe Gln Ser Leu Gln Arg Ala Leu Thr Ala Ile Arg Asp		
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Trp Leu Arg Leu Lys Ala Ala Tyr Leu Gln Tyr Gly Cys Glu Trp Ile		
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 <213> HIV-2/VCP Clone p16.5 (env)

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gagaatatta aatttaaagc accaggaaga ggctcagacc cagaagcagc atacatgtgg	840
actaactgca gaggggaatt tctctactgc gacatgactt ggttcctcaa ttgggtagat	900
aacaggacgg gtcagaaaca gcgcaattat gcaccgtgcc atataagaca aataattaat	960
acttggcaca gggtagggaa aaacgtatat ttgcctccca gggaagggga gttgacctgc	1020
aactcaacag tgaccagcat aattgccaac attgatacgg gagatcaaac agatattacc	1080
tttagtgcag aggtggcaga actataccga ttggaattgg gagattacaa attagtagaa	1140
atcacaccaa ttggcttcgc acctacatca gtaaagagat actcctctgc tcaccagaga	1200
catacaaga	1209

<210> 9  
 <211> 972  
 <212> DNA  
 <213> HIV-2/VCP Clone p16.5 (gp41)

<400> 9	
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gcgtcgggtga cgctgaccgc tcagtcccgg acttcattga ctgggatagt gcagcaacag	120
caacagctgt tggatgtggt caagaaacaa caagaaatgt tgcgactgac cgtctgggga	180
actaaaaatc tccaggcaag agtcactgct atagagaaat acctaaagga ccaggcgcag	240
ctaaattcat ggggatgtgc gtttagacaa gtctgccaca cttctgtacc atgggtaa	300
gatagcttga cacctgattg gaacaatatg acgtggcagg aatgggaaca aaaagtccgc	360
tactgggagg caaatatcag tcaaagtcta gaacaagcac aaattcagca agaaaagaat	420
ttgtatgagc tgcaaaaatt aaatagctgg ggtgttttta ccaattggct tgacttcacc	480
tcctgggtca ggtatattca atatggagtt tacgtagtag taggaatagt agctttaaga	540
atagtaatat atatagtaca gatgttaagt agacttagga agggctatag gcctgttttc	600
tcctcccccc cgggttatat ccaacagatc catatccaca aggaccagga acagccagcc	660
agagaagaaa cagaagaaga cgttggaagc aacggtggag acagatcttg gctttagccg	720
atagcatata ttcatttcct gatccgcctg ctgattcgcc tcttgatcgg gctatacaac	780
atctgcagag acttactatc caggatctcc ccgatcctcc aaccaatctt ccagagtctc	840
cagagagcac taacagcaat cagagactgg ctgaggctta aagcagccta cctgcagtat	900
gggtgcgagt ggatccaaga agcgttccaa gcccttgcaa ggactacaag agagactctt	960
gcaggcgcgg gg	972

<210> 10  
 <211> 726  
 <212> PRT  
 <213> HIV-2/VCP Clone p16.5 (env)

<400> 10

Met Lys Gly Ser Lys Asn Gln Leu Leu Ile Ala Ile Val Leu Ala Ser  
 1 5 10 15

Ala Tyr Leu Thr His Cys Lys Gln Phe Val Thr Val Phe Tyr Gly Ile  
 20 25 30

Pro Ala Trp Arg Asn Ala Ser Ile Pro Leu Phe Cys Ala Thr Lys Asn  
 35 40 45

Arg Asp Thr Trp Gly Thr Val Gln Cys Leu Pro Asp Asn Asp Asp Tyr  
 50 55 60

Gln Glu Ile Ala Leu Asn Val Thr Glu Ala Phe Asp Ala Trp Asp Asn  
 65 70 75 80

Thr Val Thr Glu Gln Ala Val Glu Asp Val Trp Asn Leu Phe Glu Thr  
 85 90 95

Ser Ile Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Gly Ala Gly  
 100 105 110

His Cys Asn Thr Ser Val Ile Lys Glu Ser Cys Asp Lys His Tyr Trp  
 115 120 125

Asp Ala Met Arg Phe Arg Tyr Cys Ala Pro Pro Gly Phe Ala Leu Leu  
 130 135 140

Arg Cys Asn Asp Ile Asn Tyr Ser Gly Phe Ala Pro Asn Cys Ser Lys  
 145 150 155 160

Val Val Ala Ala Thr Cys Thr Arg Met Met Glu Thr Gln Ser Ser Thr  
 165 170 175

Trp Phe Gly Phe Asn Gly Thr Arg Thr Glu Asn Arg Thr Tyr Ile Tyr  
 180 185 190

Trp His Gly Lys Asn Asn Arg Thr Ile Ile Ser Leu Asn Asn Phe Tyr  
195 200 205

Asn Leu Thr Met His Cys Lys Arg Pro Gly Asn Lys Gly Ala Gly Lys  
210 215 220

Pro Arg Gln Ala Trp Cys Trp Phe Lys Gly Glu Trp Lys Glu Ala Met  
225 230 235 240

Gln Glu Val Lys Glu Thr Leu Ala Lys His Pro Arg Tyr Lys Gly Asn  
245 250 255

Arg Ser Arg Thr Glu Asn Ile Lys Phe Lys Ala Pro Gly Arg Gly Ser  
260 265 270

Asp Pro Glu Ala Ala Tyr Met Trp Thr Asn Cys Arg Gly Glu Phe Leu  
275 280 285

Tyr Cys Asp Met Thr Trp Phe Leu Asn Trp Val Asp Asn Arg Thr Gly  
290 295 300

Gln Lys Gln Arg Asn Tyr Ala Pro Cys His Ile Arg Gln Ile Ile Asn  
305 310 315 320

Thr Trp His Arg Val Gly Lys Asn Val Tyr Leu Pro Pro Arg Glu Gly  
325 330 335

Glu Leu Thr Cys Asn Ser Thr Val Thr Ser Ile Ile Ala Asn Ile Asp  
340 345 350

Thr Gly Asp Gln Thr Asp Ile Thr Phe Ser Ala Glu Val Ala Glu Leu  
355 360 365

Tyr Arg Leu Glu Leu Gly Asp Tyr Lys Leu Val Glu Ile Thr Pro Ile  
370 375 380

Gly Phe Ala Pro Thr Ser Val Lys Arg Tyr Ser Ser Ala His Gln Arg  
385 390 395 400

His Thr Arg Gly Val Phe Val Leu Gly Phe Leu Gly Phe Leu Ala Thr  
405 410 415

Ala Gly Ser Ala Met Gly Ala Ala Ser Val Thr Leu Thr Ala Gln Ser



420	425	430
Arg Thr Ser Leu Thr Gly Ile Val Gln Gln Gln Gln Gln Leu Leu Asp		
435	440	445
Val Val Lys Lys Gln Gln Glu Met Leu Arg Leu Thr Val Trp Gly Thr		
450	455	460
Lys Asn Leu Gln Ala Arg Val Thr Ala Ile Glu Lys Tyr Leu Lys Asp		
465	470	475 480
Gln Ala Gln Leu Asn Ser Trp Gly Cys Ala Phe Arg Gln Val Cys His		
485	490	495
Thr Ser Val Pro Trp Val Asn Asp Ser Leu Thr Pro Asp Trp Asn Asn		
500	505	510
Met Thr Trp Gln Glu Trp Glu Gln Lys Val Arg Tyr Trp Glu Ala Asn		
515	520	525
Ile Ser Gln Ser Leu Glu Gln Ala Gln Ile Gln Gln Glu Lys Asn Leu		
530	535	540
Tyr Glu Leu Gln Lys Leu Asn Ser Trp Gly Val Phe Thr Asn Trp Leu		
545	550	555 560
Asp Phe Thr Ser Trp Val Arg Tyr Ile Gln Tyr Gly Val Tyr Val Val		
565	570	575
Val Gly Ile Val Ala Leu Arg Ile Val Ile Tyr Ile Val Gln Met Leu		
580	585	590
Ser Arg Leu Arg Lys Gly Tyr Arg Pro Val Phe Ser Ser Pro Pro Gly		
595	600	605
Tyr Ile Gln Gln Ile His Ile His Lys Asp Gln Glu Gln Pro Ala Arg		
610	615	620
Glu Glu Thr Glu Glu Asp Val Gly Ser Asn Gly Gly Asp Arg Ser Trp		
625	630	635 640
Leu Pro Ile Ala Tyr Ile His Phe Leu Ile Arg Leu Leu Ile Arg Leu		
645	650	655

Leu Ile Gly Leu Tyr Asn Ile Cys Arg Asp Leu Leu Ser Arg Ile Ser  
660 665 670

Pro Ile Leu Gln Pro Ile Phe Gln Ser Leu Gln Arg Ala Leu Thr Ala  
675 680 685

Ile Arg Asp Trp Leu Arg Leu Lys Ala Ala Tyr Leu Gln Tyr Gly Cys  
690 695 700

Glu Trp Ile Gln Glu Ala Phe Gln Ala Leu Ala Arg Thr Thr Arg Glu  
705 710 715 720

Thr Leu Ala Gly Ala Gly  
725

<210> 11  
<211> 403  
<212> PRT  
<213> HIV-2/VCP Clone p16.5 (gp120)

<400> 11

Met Lys Gly Ser Lys Asn Gln Leu Leu Ile Ala Ile Val Leu Ala Ser  
1 5 10 15

Ala Tyr Leu Thr His Cys Lys Gln Phe Val Thr Val Phe Tyr Gly Ile  
20 25 30

Pro Ala Trp Arg Asn Ala Ser Ile Pro Leu Phe Cys Ala Thr Lys Asn  
35 40 45

Arg Asp Thr Trp Gly Thr Val Gln Cys Leu Pro Asp Asn Asp Asp Tyr  
50 55 60

Gln Glu Ile Ala Leu Asn Val Thr Glu Ala Phe Asp Ala Trp Asp Asn  
65 70 75 80

Thr Val Thr Glu Gln Ala Val Glu Asp Val Trp Asn Leu Phe Glu Thr  
85 90 95

Ser Ile Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Gly Ala Gly  
100 105 110

His Cys Asn Thr Ser Val Ile Lys Glu Ser Cys Asp Lys His Tyr Trp  
115 120 125

Asp Ala Met Arg Phe Arg Tyr Cys Ala Pro Pro Gly Phe Ala Leu Leu  
130 135 140

Arg Cys Asn Asp Ile Asn Tyr Ser Gly Phe Ala Pro Asn Cys Ser Lys  
145 150 155 160

Val Val Ala Ala Thr Cys Thr Arg Met Met Glu Thr Gln Ser Ser Thr  
165 170 175

Trp Phe Gly Phe Asn Gly Thr Arg Thr Glu Asn Arg Thr Tyr Ile Tyr  
180 185 190

Trp His Gly Lys Asn Asn Arg Thr Ile Ile Ser Leu Asn Asn Phe Tyr  
195 200 205

Asn Leu Thr Met His Cys Lys Arg Pro Gly Asn Lys Gly Ala Gly Lys  
210 215 220

Pro Arg Gln Ala Trp Cys Trp Phe Lys Gly Glu Trp Lys Glu Ala Met  
225 230 235 240

Gln Glu Val Lys Glu Thr Leu Ala Lys His Pro Arg Tyr Lys Gly Asn  
245 250 255

Arg Ser Arg Thr Glu Asn Ile Lys Phe Lys Ala Pro Gly Arg Gly Ser  
260 265 270

Asp Pro Glu Ala Ala Tyr Met Trp Thr Asn Cys Arg Gly Glu Phe Leu  
275 280 285

Tyr Cys Asp Met Thr Trp Phe Leu Asn Trp Val Asp Asn Arg Thr Gly  
290 295 300

Gln Lys Gln Arg Asn Tyr Ala Pro Cys His Ile Arg Gln Ile Ile Asn  
305 310 315 320

Thr Trp His Arg Val Gly Lys Asn Val Tyr Leu Pro Pro Arg Glu Gly  
325 330 335

Glu Leu Thr Cys Asn Ser Thr Val Thr Ser Ile Ile Ala Asn Ile Asp

340                      345                      350  
 Thr Gly Asp Gln Thr Asp Ile Thr Phe Ser Ala Glu Val Ala Glu Leu  
           355                      360                      365  
 Tyr Arg Leu Glu Leu Gly Asp Tyr Lys Leu Val Glu Ile Thr Pro Ile  
           370                      375                      380  
 Gly Phe Ala Pro Thr Ser Val Lys Arg Tyr Ser Ser Ala His Gln Arg  
 385                      390                      395                      400  
 His Thr Arg

<210> 12  
 <211> 323  
 <212> PRT  
 <213> HIV-2/VCP Clone p16.5 (gp41)

<400> 12

Gly Val Phe Val Leu Gly Phe Leu Gly Phe Leu Ala Thr Ala Gly Ser  
 1                      5                      10                      15  
 Ala Met Gly Ala Ala Ser Val Thr Leu Thr Ala Gln Ser Arg Thr Ser  
           20                      25                      30  
 Leu Thr Gly Ile Val Gln Gln Gln Gln Gln Leu Leu Asp Val Val Lys  
           35                      40                      45  
 Lys Gln Gln Glu Met Leu Arg Leu Thr Val Trp Gly Thr Lys Asn Leu  
           50                      55                      60  
 Gln Ala Arg Val Thr Ala Ile Glu Lys Tyr Leu Lys Asp Gln Ala Gln  
 65                      70                      75                      80  
 Leu Asn Ser Trp Gly Cys Ala Phe Arg Gln Val Cys His Thr Ser Val  
           85                      90                      95  
 Pro Trp Val Asn Asp Ser Leu Thr Pro Asp Trp Asn Asn Met Thr Trp  
           100                      105                      110  
 Gln Glu Trp Glu Gln Lys Val Arg Tyr Trp Glu Ala Asn Ile Ser Gln  
           115                      120                      125

Ser Leu Glu Gln Ala Gln Ile Gln Gln Glu Lys Asn Leu Tyr Glu Leu  
130 135 140

Gln Lys Leu Asn Ser Trp Gly Val Phe Thr Asn Trp Leu Asp Phe Thr  
145 150 155 160

Ser Trp Val Arg Tyr Ile Gln Tyr Gly Val Tyr Val Val Val Gly Ile  
165 170 175

Val Ala Leu Arg Ile Val Ile Tyr Ile Val Gln Met Leu Ser Arg Leu  
180 185 190

Arg Lys Gly Tyr Arg Pro Val Phe Ser Ser Pro Pro Gly Tyr Ile Gln  
195 200 205

Gln Ile His Ile His Lys Asp Gln Glu Gln Pro Ala Arg Glu Glu Thr  
210 215 220

Glu Glu Asp Val Gly Ser Asn Gly Gly Asp Arg Ser Trp Leu Pro Ile  
225 230 235 240

Ala Tyr Ile His Phe Leu Ile Arg Leu Leu Ile Arg Leu Leu Ile Gly  
245 250 255

Leu Tyr Asn Ile Cys Arg Asp Leu Leu Ser Arg Ile Ser Pro Ile Leu  
260 265 270

Gln Pro Ile Phe Gln Ser Leu Gln Arg Ala Leu Thr Ala Ile Arg Asp  
275 280 285

Trp Leu Arg Leu Lys Ala Ala Tyr Leu Gln Tyr Gly Cys Glu Trp Ile  
290 295 300

Gln Glu Ala Phe Gln Ala Leu Ala Arg Thr Thr Arg Glu Thr Leu Ala  
305 310 315 320

Gly Ala Gly

<210> 13  
<211> 1926  
<212> DNA  
<213> HIV-2/VCP Clone p16.7 (env)

<400> 13

atgaagggtgta gtaagaatca accgctgatt gctattgtac tagctagtgc ttacctaaca	60
cattgcaagc aatttgtgac tgttttctat ggcatacccg cgtggaggaa tgcattccatt	120
cccctgtttt gtgcaaccaa aaatagagat acttggggaa ccgtacagtg cttgccagac	180
aatgatgatt atcaggaaat agctttaaat gtaacagagg ctttcgatgc atgggataat	240
acagtaacag aacaagcagt ggaggatgtc tggaatctat ctgagacatc aataaaacca	300
tgtgtcaaat taacaccctt atgtgtaggt gccggccatt gcaatacatc agtcatcaca	360
gagtcagtgtg ataagcacta ttgggatgct atgaggttta gatactgtgc accaccgggt	420
tttgccttac taagatgcaa tgataactaat tattcaggct ttgcacctaa ttgctctaaa	480
gtagtagctg ctacatgcac cagaatgatg gaaacgcaat cttctacatg gtttggcttt	540
aatggcacta gagcagaaaa tagaacatat atctattggc atggtaaaaa tgacagaact	600
attatcagct taaataactt ttataatctc actatgcatt gtaagaggcc gggaaataag	660
ggtgccggca aaccaggca agcatggtgt tggttcaaag gcgaatggaa ggaagccatg	720
caggagggtga aggagaccct tgcgaaacat cctagatata aagggaacag gagccgcaca	780
gagaatatta aatttaaagc accaggaaga ggctcagacc cagaagcagc atacatgtgg	840
actaactgca gaggggaatt tctctactgc gacatgactt ggttcctcaa ttgggtagaa	900
aacaggacgg gtcagaaaca gcgtaattat gcaccgtgcc atataaggca aataattaat	960
acttggcaca gggtagggaa aaacgtatat ttgcctccca gggaaagggga gttaacctgc	1020
aactcaacag tgaccagcat aattgccaac attgatacgg gagatcaaac agatattacc	1080
tttagtgagc aggtggcaga actataccgg ttggaattgg gagattacaa attagtagaa	1140
atcacaccaa ttggcttcgc acctacatca gtaaagagat actcctctgc tcaccagaga	1200
catacaagag gtgtgttcgt gctagggttc ttgggttttc tcgcaacggc aggttctgca	1260
atgggcgcgg cgtcggtgac gctgaccgct cagtcccga cttcattgac tggggtagtg	1320
cagcaacagc aacagctgtt ggatgtggtc aagaaacaac aagaaatgtt gcgactgacc	1380
gtctggggaa ctaaaaatct ccaggcaaga gtcactgcta tagagaaata cctaaaggac	1440
caggcgcagc taaattcatg gggatgtgcg tttagacaag tctgccacac ttctgtacca	1500
tgggtaaatg atagcttgac acctgattgg aacaatatga cgtggcagga atgggaacaa	1560
aaagtccgct actgggaggc aaatatcagt caaagtctag aacaagcaca aattcagcaa	1620
gaaaagaatt tgtatgagct gcaaaaatta aatagctggg gtgtttttac caattggctt	1680

gacttcacct cctgggtcag gtatatattcaa tatggagttt atgtagtagt aggaatagta	1740
gctttaagaa tagtaatata tatagtacag atgttgagta gacttaggaa gggctatagg	1800
cctgttttct cctccccccc cggttatatc caacagatcc atatccacaa ggaccaggaa	1860
cagccagcca gagaagaaac agaagaagac gttggaagca acggtggaga caaatcttgg	1920
ctttag	1926

<210> 14  
 <211> 1209  
 <212> DNA  
 <213> HIV-2/VCP Clone p16.7 (gp120)

<400> 14	
atgaagggtgta gtaagaatca accgctgatt gctattgtac tagctagtgc ttacctaaca	60
cattgcaagc aatttgtgac tgttttctat ggcataccgc cgtggaggaa tgcattccatt	120
cccctgtttt gtgcaaccaa aaatagagat acttggggaa ccgtacagtg cttgccagac	180
aatgatgatt atcaggaaat agctttaaat gtaacagagg ctttcgatgc atgggataat	240
acagtaacag aacaagcagt ggaggatgtc tggaatctat ctgagacatc aataaaacca	300
tgtgtcaaata taacaccctt atgtgtaggt gccggccatt gcaatacatc agtcatacaca	360
gagtcagtgtg ataagcacta ttgggatgct atgaggttta gatactgtgc accaccgggt	420
tttgccttac taagatgcaa tgataactat tattcaggct ttgcacctaa ttgctctaaa	480
gtagtagctg ctacatgcac cagaatgatg gaaacgcaat cttctacatg gtttggtctt	540
aatggcacta gagcagaaaa tagaacatat atctattggc atggtaaaaa tgacagaact	600
attatcagct taaataactt ttataatctc actatgcatt gtaagaggcc gggaaataag	660
gggtgccggca aaccaggca agcatggtgt tggttcaaag gcgaatggaa ggaagccatg	720
caggaggtga aggagaccct tgcgaaacat cctagatata aagggaacag gagccgcaca	780
gagaatatta aatttaaagc accaggaaga ggctcagacc cagaagcagc atacatgtgg	840
actaactgca gaggggaatt tctctactgc gacatgactt ggttcctcaa ttgggtagaa	900
aacaggacgg gtcagaaaca gcgtaattat gcaccgtgcc atataaggca aataattaat	960
acttggcaca gggtagggaa aaacgtatat ttgcctcca gggaagggga gttaacctgc	1020
aactcaacag tgaccagcat aattgccaac attgatacgg gagatcaaac agatattacc	1080
tttagtgcag aggtggcaga actataaccgg ttggaattgg gagattacaa attagtagaa	1140
atcacaccaa ttggcttcgc acctacatca gtaaagagat actcctctgc tcaccagaga	1200

catacaaga

1209

<210> 15  
<211> 717  
<212> DNA  
<213> HIV-2/VCP Clone p16.7 (gp41)

<400> 15  
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gcgtcgggtga cgctgaccgc tcagtcccgg acttcattga ctggggtagt gcagcaacag 120  
caacagctgt tggatgtggt caagaaacaa caagaaatgt tgcgactgac cgtctgggga 180  
actaaaaatc tccaggcaag agtcactgct atagagaaat acctaaagga ccaggcgcag 240  
ctaaattcat ggggatgtgc gtttagacaa gtctgccaca cttctgtacc atgggtaaat 300  
gatagcttga cacctgattg gaacaatatg acgtggcagg aatgggaaca aaaagtccgc 360  
tactgggagg caaatatcag tcaaagtcta gaacaagcac aaattcagca agaaaagaat 420  
ttgtatgagc tgcaaaaatt aaatagctgg ggtgttttta ccaattggct tgacttcacc 480  
tcctgggtca ggtatattca atatggagtt tatgtagtag taggaatagt agctttaaga 540  
atagtaatat atatagtaca gatgttgagt agacttagga agggctatag gcctgttttc 600  
tcctcccccc ccggttatat ccaacagatc catatccaca aggaccagga acagccagcc 660  
agagaagaaa cagaagaaga cgttggaagc aacggtggag acaaatcttg gcttttag 717

<210> 16  
<211> 641  
<212> PRT  
<213> HIV-2/VCP Clone p16.7 (env)

<400> 16

Met Lys Gly Ser Lys Asn Gln Pro Leu Ile Ala Ile Val Leu Ala Ser  
1 5 10 15

Ala Tyr Leu Thr His Cys Lys Gln Phe Val Thr Val Phe Tyr Gly Ile  
20 25 30

Pro Ala Trp Arg Asn Ala Ser Ile Pro Leu Phe Cys Ala Thr Lys Asn  
35 40 45

Arg Asp Thr Trp Gly Thr Val Gln Cys Leu Pro Asp Asn Asp Asp Tyr  
50 55 60



Gln Glu Ile Ala Leu Asn Val Thr Glu Ala Phe Asp Ala Trp Asp Asn  
65 70 75 80

Thr Val Thr Glu Gln Ala Val Glu Asp Val Trp Asn Leu Ser Glu Thr  
85 90 95

Ser Ile Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Gly Ala Gly  
100 105 110

His Cys Asn Thr Ser Val Ile Thr Glu Ser Cys Asp Lys His Tyr Trp  
115 120 125

Asp Ala Met Arg Phe Arg Tyr Cys Ala Pro Pro Gly Phe Ala Leu Leu  
130 135 140

Arg Cys Asn Asp Thr Asn Tyr Ser Gly Phe Ala Pro Asn Cys Ser Lys  
145 150 155 160

Val Val Ala Ala Thr Cys Thr Arg Met Met Glu Thr Gln Ser Ser Thr  
165 170 175

Trp Phe Gly Phe Asn Gly Thr Arg Ala Glu Asn Arg Thr Tyr Ile Tyr  
180 185 190

Trp His Gly Lys Asn Asp Arg Thr Ile Ile Ser Leu Asn Asn Phe Tyr  
195 200 205

Asn Leu Thr Met His Cys Lys Arg Pro Gly Asn Lys Gly Ala Gly Lys  
210 215 220

Pro Arg Gln Ala Trp Cys Trp Phe Lys Gly Glu Trp Lys Glu Ala Met  
225 230 235 240

Gln Glu Val Lys Glu Thr Leu Ala Lys His Pro Arg Tyr Lys Gly Asn  
245 250 255

Arg Ser Arg Thr Glu Asn Ile Lys Phe Lys Ala Pro Gly Arg Gly Ser  
260 265 270

Asp Pro Glu Ala Ala Tyr Met Trp Thr Asn Cys Arg Gly Glu Phe Leu  
275 280 285

Tyr Cys Asp Met Thr Trp Phe Leu Asn Trp Val Glu Asn Arg Thr Gly  
 290 295 300

Gln Lys Gln Arg Asn Tyr Ala Pro Cys His Ile Arg Gln Ile Ile Asn  
 305 310 315 320

Thr Trp His Arg Val Gly Lys Asn Val Tyr Leu Pro Pro Arg Glu Gly  
 325 330 335

Glu Leu Thr Cys Asn Ser Thr Val Thr Ser Ile Ile Ala Asn Ile Asp  
 340 345 350

Thr Gly Asp Gln Thr Asp Ile Thr Phe Ser Ala Glu Val Ala Glu Leu  
 355 360 365

Tyr Arg Leu Glu Leu Gly Asp Tyr Lys Leu Val Glu Ile Thr Pro Ile  
 370 375 380

Gly Phe Ala Pro Thr Ser Val Lys Arg Tyr Ser Ser Ala His Gln Arg  
 385 390 395 400

His Thr Arg Gly Val Phe Val Leu Gly Phe Leu Gly Phe Leu Ala Thr  
 405 410 415

Ala Gly Ser Ala Met Gly Ala Ala Ser Val Thr Leu Thr Ala Gln Ser  
 420 425 430

Arg Thr Ser Leu Thr Gly Val Val Gln Gln Gln Gln Gln Leu Leu Asp  
 435 440 445

Val Val Lys Lys Gln Gln Glu Met Leu Arg Leu Thr Val Trp Gly Thr  
 450 455 460

Lys Asn Leu Gln Ala Arg Val Thr Ala Ile Glu Lys Tyr Leu Lys Asp  
 465 470 475 480

Gln Ala Gln Leu Asn Ser Trp Gly Cys Ala Phe Arg Gln Val Cys His  
 485 490 495

Thr Ser Val Pro Trp Val Asn Asp Ser Leu Thr Pro Asp Trp Asn Asn  
 500 505 510

Met Thr Trp Gln Glu Trp Glu Gln Lys Val Arg Tyr Trp Glu Ala Asn

515

520

525

Ile Ser Gln Ser Leu Glu Gln Ala Gln Ile Gln Gln Glu Lys Asn Leu  
 530 535 540

Tyr Glu Leu Gln Lys Leu Asn Ser Trp Gly Val Phe Thr Asn Trp Leu  
 545 550 555 560

Asp Phe Thr Ser Trp Val Arg Tyr Ile Gln Tyr Gly Val Tyr Val Val  
 565 570 575

Val Gly Ile Val Ala Leu Arg Ile Val Ile Tyr Ile Val Gln Met Leu  
 580 585 590

Ser Arg Leu Arg Lys Gly Tyr Arg Pro Val Phe Ser Ser Pro Pro Gly  
 595 600 605

Tyr Ile Gln Gln Ile His Ile His Lys Asp Gln Glu Gln Pro Ala Arg  
 610 615 620

Glu Glu Thr Glu Glu Asp Val Gly Ser Asn Gly Gly Asp Lys Ser Trp  
 625 630 635 640

Leu

<210> 17  
 <211> 403  
 <212> PRT  
 <213> HIV-2/VCP Clone p16.7 (gp120)

<400> 17

Met Lys Gly Ser Lys Asn Gln Pro Leu Ile Ala Ile Val Leu Ala Ser  
 1 5 10 15

Ala Tyr Leu Thr His Cys Lys Gln Phe Val Thr Val Phe Tyr Gly Ile  
 20 25 30

Pro Ala Trp Arg Asn Ala Ser Ile Pro Leu Phe Cys Ala Thr Lys Asn  
 35 40 45

Arg Asp Thr Trp Gly Thr Val Gln Cys Leu Pro Asp Asn Asp Asp Tyr  
 50 55 60

Gln Glu Ile Ala Leu Asn Val Thr Glu Ala Phe Asp Ala Trp Asp Asn  
65 70 75 80

Thr Val Thr Glu Gln Ala Val Glu Asp Val Trp Asn Leu Ser Glu Thr  
85 90 95

Ser Ile Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Gly Ala Gly  
100 105 110

His Cys Asn Thr Ser Val Ile Thr Glu Ser Cys Asp Lys His Tyr Trp  
115 120 125

Asp Ala Met Arg Phe Arg Tyr Cys Ala Pro Pro Gly Phe Ala Leu Leu  
130 135 140

Arg Cys Asn Asp Thr Asn Tyr Ser Gly Phe Ala Pro Asn Cys Ser Lys  
145 150 155 160

Val Val Ala Ala Thr Cys Thr Arg Met Met Glu Thr Gln Ser Ser Thr  
165 170 175

Trp Phe Gly Phe Asn Gly Thr Arg Ala Glu Asn Arg Thr Tyr Ile Tyr  
180 185 190

Trp His Gly Lys Asn Asp Arg Thr Ile Ile Ser Leu Asn Asn Phe Tyr  
195 200 205

Asn Leu Thr Met His Cys Lys Arg Pro Gly Asn Lys Gly Ala Gly Lys  
210 215 220

Pro Arg Gln Ala Trp Cys Trp Phe Lys Gly Glu Trp Lys Glu Ala Met  
225 230 235 240

Gln Glu Val Lys Glu Thr Leu Ala Lys His Pro Arg Tyr Lys Gly Asn  
245 250 255

Arg Ser Arg Thr Glu Asn Ile Lys Phe Lys Ala Pro Gly Arg Gly Ser  
260 265 270

Asp Pro Glu Ala Ala Tyr Met Trp Thr Asn Cys Arg Gly Glu Phe Leu  
275 280 285

Tyr Cys Asp Met Thr Trp Phe Leu Asn Trp Val Glu Asn Arg Thr Gly  
 290 295 300

Gln Lys Gln Arg Asn Tyr Ala Pro Cys His Ile Arg Gln Ile Ile Asn  
 305 310 315 320

Thr Trp His Arg Val Gly Lys Asn Val Tyr Leu Pro Pro Arg Glu Gly  
 325 330 335

Glu Leu Thr Cys Asn Ser Thr Val Thr Ser Ile Ile Ala Asn Ile Asp  
 340 345 350

Thr Gly Asp Gln Thr Asp Ile Thr Phe Ser Ala Glu Val Ala Glu Leu  
 355 360 365

Tyr Arg Leu Glu Leu Gly Asp Tyr Lys Leu Val Glu Ile Thr Pro Ile  
 370 375 380

Gly Phe Ala Pro Thr Ser Val Lys Arg Tyr Ser Ser Ala His Gln Arg  
 385 390 395 400

His Thr Arg

<210> 18  
 <211> 238  
 <212> PRT  
 <213> HIV-2/VCP Clone p16.7 (gp41)

<400> 18

Gly Val Phe Val Leu Gly Phe Leu Gly Phe Leu Ala Thr Ala Gly Ser  
 1 5 10 15

Ala Met Gly Ala Ala Ser Val Thr Leu Thr Ala Gln Ser Arg Thr Ser  
 20 25 30

Leu Thr Gly Val Val Gln Gln Gln Gln Leu Leu Asp Val Val Lys  
 35 40 45

Lys Gln Gln Glu Met Leu Arg Leu Thr Val Trp Gly Thr Lys Asn Leu  
 50 55 60

Gln Ala Arg Val Thr Ala Ile Glu Lys Tyr Leu Lys Asp Gln Ala Gln  
 65 70 75 80

Leu Asn Ser Trp Gly Cys Ala Phe Arg Gln Val Cys His Thr Ser Val  
85 90 95

Pro Trp Val Asn Asp Ser Leu Thr Pro Asp Trp Asn Asn Met Thr Trp  
100 105 110

Gln Glu Trp Glu Gln Lys Val Arg Tyr Trp Glu Ala Asn Ile Ser Gln  
115 120 125

Ser Leu Glu Gln Ala Gln Ile Gln Gln Glu Lys Asn Leu Tyr Glu Leu  
130 135 140

Gln Lys Leu Asn Ser Trp Gly Val Phe Thr Asn Trp Leu Asp Phe Thr  
145 150 155 160

Ser Trp Val Arg Tyr Ile Gln Tyr Gly Val Tyr Val Val Val Gly Ile  
165 170 175

Val Ala Leu Arg Ile Val Ile Tyr Ile Val Gln Met Leu Ser Arg Leu  
180 185 190

Arg Lys Gly Tyr Arg Pro Val Phe Ser Ser Pro Pro Gly Tyr Ile Gln  
195 200 205

Gln Ile His Ile His Lys Asp Gln Glu Gln Pro Ala Arg Glu Glu Thr  
210 215 220

Glu Glu Asp Val Gly Ser Asn Gly Gly Asp Lys Ser Trp Leu  
225 230 235

<210> 19  
<211> 2427  
<212> DNA  
<213> HIV-2/VCP Clone p16.9 (env)

<400> 19  
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cattgcaagc aatttgtgac tgttttctat ggcataccgc cgtggaggaa tgcattccatt 120  
ccccctgtttt gtgcaaccaa aaatagagat acttgggggaa ccatacagtg cttgccagac 180  
aatgatgatt atcaggaaat agctctaaat gtaacagagg ctttcgatgc atggaataat 240  
acagtaacag aacaagcagt ggaggatgtc tggaatctat ttgagacatc aataaaacca 300

tgtgtcaa	at	taacaccctt	atgtgtagca	atgaactgta	caaggaacat	gaccacatcc	360
acagggacca	cagacaccca	aaatatcaca	attataaatg	acacttcgcc	atgcgtacgt		420
gcagacaact	gcacaggatt	aaaggaggaa	gaaatggtcg	actgtcagtt	taatatgaca		480
ggattagaga	gagacaagag	aaaacagtat	actggagcat	ggtactcaaa	agatgtgatt		540
tgtgacaata	acacctcaag	tcggagcaag	tgttacatga	accattgcaa	tacatcagtc		600
atcacagagt	catgtgataa	gcactattgg	gatgctatga	ggttttagata	ctgtgcacca		660
ccgggttttg	ccctactaag	atgcaatgat	actaattatt	caggctttgc	acctaattgc		720
tctaaagtag	tagctgctac	atgcaccaga	atgatggaaa	cgcaatcttc	tacatggttt		780
ggatttaatg	gcactagagc	agaaaaataga	acatatatct	attggcatgg	taaaaataac		840
agaactatta	tcagcttaaa	taacttttat	aatctcacta	tgcattgtaa	gaggccggga		900
aataagggtg	ccggcaaacc	caggcaagca	tggtgttgg	tcaaaggcga	atggaaggaa		960
gccatgcagg	aggtgaagga	gacccttgcg	aaacatccca	gatataaagg	gaacaggagc		1020
cgcacagaga	atattaaatt	taaagcacca	ggaagaggct	cagacccaga	agcagcatat		1080
atgtggacta	actgcagagg	ggaatttctc	tactgcaaca	tggttggtt	cctcaattgg		1140
gtagataaca	ggacgggtca	gaaacagcgc	aattatgcac	cgtgccatat	aaggcaaata		1200
attaatactt	ggcacagggt	agggaaaaac	atatatttgc	ctcccaggga	aggggagttg		1260
acctgcaact	caacagtgac	cagcataatt	gccaacattg	atacgggaga	tcaaacagat		1320
attaccttta	gtgcagaggt	ggcagaacta	taccgattgg	aattgggaga	ttacaaatta		1380
gtagaaatca	caccaattgg	cttcgcacct	acatcagtaa	agagatactc	ctctgctcac		1440
cagagacata	caagagggtg	gttcgtgcta	gggttcttgg	gttttctcgc	aacggcaggt		1500
tctgcaatgg	gcgcggcgct	ggtgacgctg	accgcccagt	cccggacttc	attggctggg		1560
atagtgcagc	aacagcaaca	gctgttggac	gtgggtcaaga	aacaacaaga	aatgttgcca		1620
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aaggaccagg	cgcagttaaa	ttcatgggga	tgtgcgttta	gacaagtctg	ccacacttct		1740
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gaacagaaaag	tccgctactg	ggaggcaaat	atcagtcaaa	gtctagaaca	agcacaaatt		1860
cagcaagaaa	agaatttgta	tgagctgcaa	aaattaaata	gctgggggtg	ttttaccaat		1920
tggttgact	tcacctctg	ggtcagggtat	attcaatatg	gagtttatgt	agtagtagga		1980

atagtaactt taagaatagt aatatatata gtacagatgt taagtagact taggaagggc	2040
tataggcctg ttttctctc ccccccggt tatatccaac agatccatat ccacaaggac	2100
caggaacagc cagccagaga agaaacagaa gaagacgttg gaagcaacgg tggagacaga	2160
tcttggcttt agccgatagc atatattcat ttcctgatcc gcctgctgat tcgcctcttg	2220
atcgggctat acaacatctg cagagactta ctatccagga tctccccgat cctccaacca	2280
atcttccaga gtctccagag agcactaaca gcaatcagag actggctgag gcttaaagca	2340
gcctacctgc agtatgggtg cgagtggatc caagaagcgt tccaagccct tgcaaggact	2400
acaagagaga ctcttgagg cgcgggg	2427

<210> 20  
 <211> 1455  
 <212> DNA  
 <213> HIV-2/VCP Clone p16.9 (gp120)

<400> 20	
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cattgcaagc aatttgtgac tgttttctat ggcatacccg cgtggaggaa tgcattccatt	120
cccctgtttt gtgcaaccaa aaatagagat acttggggaa ccatacagtg cttgccagac	180
aatgatgatt atcaggaaat agctctaaat gtaacagagg ctttcgatgc atggaataat	240
acagtaacag aacaagcagt ggaggatgtc tggaatctat ttgagacatc aataaaacca	300
tgtgtcaaat taacaccctt atgtgtagca atgaactgta caaggaacat gaccacatcc	360
acagggacca cagacacca aaatatcaca attataaatg acacttcgcc atgcgtacgt	420
gcagacaact gcacaggatt aaaggaggaa gaaatggtcg actgtcagtt taatatgaca	480
ggattagaga gagacaagag aaaacagtat actggagcat ggtactcaa agatgtgatt	540
tgtgacaata acacctcaag tcggagcaag tgttacatga accattgcaa tacatcagtc	600
atcacagagt catgtgataa gcactattgg gatgctatga ggtttagata ctgtgcacca	660
ccgggttttg ccctactaag atgcaatgat actaattatt caggctttgc acctaatgc	720
tctaaagtag tagctgctac atgcaccaga atgatggaaa cgcaatcttc tacatggttt	780
ggatttaatg gcactagagc agaaaataga acatatatct attggcatgg taaaaataac	840
agaactatta tcagcttaaa taacttttat aatctcacta tgcattgtaa gaggccggga	900
aataaggggtg ccggcaaacc caggcaagca tgggtgttgg tcaaaggcga atggaaggaa	960
gcatgcagg aggtgaagga gacccttgcg aaacatccca gatataaagg gaacaggagc	1020



cgcacagaga atattaaatt taaagcacca ggaagaggct cagacccaga agcagcatac 1080  
atgtggacta actgcagagg ggaattttctc tactgcaaca tggcttggtt cctcaattgg 1140  
gtagataaca ggacgggtca gaaacagcgc aattatgcac cgtgccatat aaggcaaata 1200  
attaatactt ggcacagggt agggaaaaaac atatatttgc ctcccaggga aggggagttg 1260  
acctgcaact caacagtgac cagcataatt gccaacattg atacgggaga tcaaacagat 1320  
attaccttta gtgcagagggt ggcagaacta taccgattgg aattgggaga ttacaaatta 1380  
gtagaaatca caccaattgg cttcgcacct acatcagtaa agagatactc ctctgctcac 1440  
cagagacata caaga 1455

<210> 21  
<211> 717  
<212> DNA  
<213> HIV-2/VCP Clone p16.9 (gp41)

<400> 21  
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gcgtcgggtga cgctgaccgc ccagtcccggt acttcattgg ctgggatagt gcagcaacag 120  
caacagctgt tggacgtggt caagaaacaa caagaaatgt tgcgactgac cgtctgggga 180  
actaaaaatc tccagacaag agtcactgct atagagaaat acctaaagga ccaggcgcag 240  
ttaaattcat ggggatgtgc gtttagacaa gtctgccaca cttctgtacc atgggtaaata 300  
gatagcttga cacctgattg gaacaatatg acgtggcagg aatgggaaca gaaagtccgc 360  
tactgggagg caaatatcag.tcaaagtcta gaacaagcac aaattcagca agaaaagaat 420  
ttgtatgagc tgcaaaaatt aaatagctgg ggtgttttta ccaattggct tgacttcacc 480  
tcctgggtca ggtatattca atatggagtt tatgtagtag taggaatagt aactttaaga 540  
atagtaatat atatagtaca gatgttaagt agacttagga agggctatag gcctgttttc 600  
tcctcccccc ccggttatat ccaacagatc catatccaca aggaccagga acagccagcc 660  
agagaagaaa cagaagaaga cgttggaagc aacggtggag acagatcttg gcttttag 717

<210> 22  
<211> 723  
<212> PRT  
<213> HIV-2/VCP Clone p16.9 (env)

<400> 22

Met Lys Gly Ser Lys Asn Gln Leu Leu Ile Ala Ile Ile Leu Ala Ser  
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Ala Tyr Leu Thr His Cys Lys Gln Phe Val Thr Val Phe Tyr Gly Ile  
 20 25 30

Pro Ala Trp Arg Asn Ala Ser Ile Pro Leu Phe Cys Ala Thr Lys Asn  
 35 40 45

Arg Asp Thr Trp Gly Thr Ile Gln Cys Leu Pro Asp Asn Asp Asp Tyr  
 50 55 60

Gln Glu Ile Ala Leu Asn Val Thr Glu Ala Phe Asp Ala Trp Asn Asn  
 65 70 75 80

Thr Val Thr Glu Gln Ala Val Glu Asp Val Trp Asn Leu Phe Glu Thr  
 85 90 95

Ser Ile Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Ala Met Asn  
 100 105 110

Cys Thr Arg Asn Met Thr Thr Ser Thr Gly Thr Thr Asp Thr Gln Asn  
 115 120 125

Ile Thr Ile Ile Asn Asp Thr Ser Pro Cys Val Arg Ala Asp Asn Cys  
 130 135 140

Thr Gly Leu Lys Glu Glu Glu Met Val Asp Cys Gln Phe Asn Met Thr  
 145 150 155 160

Gly Leu Glu Arg Asp Lys Arg Lys Gln Tyr Thr Gly Ala Trp Tyr Ser  
 165 170 175

Lys Asp Val Ile Cys Asp Asn Asn Thr Ser Ser Arg Ser Lys Cys Tyr  
 180 185 190

Met Asn His Cys Asn Thr Ser Val Ile Thr Glu Ser Cys Asp Lys His  
 195 200 205

Tyr Trp Asp Ala Met Arg Phe Arg Tyr Cys Ala Pro Pro Gly Phe Ala  
 210 215 220

Leu Leu Arg Cys Asn Asp Thr Asn Tyr Ser Gly Phe Ala Pro Asn Cys  
 225 230 235 240

Ser Lys Val Val Ala Ala Thr Cys Thr Arg Met Met Glu Thr Gln Ser  
245 250 255

Ser Thr Trp Phe Gly Phe Asn Gly Thr Arg Ala Glu Asn Arg Thr Tyr  
260 265 270

Ile Tyr Trp His Gly Lys Asn Asn Arg Thr Ile Ile Ser Leu Asn Asn  
275 280 285

Phe Tyr Asn Leu Thr Met His Cys Lys Arg Pro Gly Asn Lys Gly Ala  
290 295 300

Gly Lys Pro Arg Gln Ala Trp Cys Trp Phe Lys Gly Glu Trp Lys Glu  
305 310 315 320

Ala Met Gln Glu Val Lys Glu Thr Leu Ala Lys His Pro Arg Tyr Lys  
325 330 335

Gly Asn Arg Ser Arg Thr Glu Asn Ile Lys Phe Lys Ala Pro Gly Arg  
340 345 350

Gly Ser Asp Pro Glu Ala Ala Tyr Met Trp Thr Asn Cys Arg Gly Glu  
355 360 365

Phe Leu Tyr Cys Asn Met Ala Trp Phe Leu Asn Trp Val Asp Asn Arg  
370 375 380

Thr Gly Gln Lys Gln Arg Asn Tyr Ala Pro Cys His Ile Arg Gln Ile  
385 390 395 400

Ile Asn Thr Trp His Arg Val Gly Lys Asn Ile Tyr Leu Pro Pro Arg  
405 410 415

Glu Gly Glu Leu Thr Cys Asn Ser Thr Val Thr Ser Ile Ile Ala Asn  
420 425 430

Ile Asp Thr Gly Asp Gln Thr Asp Ile Thr Phe Ser Ala Glu Val Ala  
435 440 445

Glu Leu Tyr Arg Leu Glu Leu Gly Asp Tyr Lys Leu Val Glu Ile Thr  
450 455 460

Pro Ile Gly Phe Ala Pro Thr Ser Val Lys Arg Tyr Ser Ser Ala His  
 465 470 475 480

Gln Arg His Thr Arg Gly Val Phe Val Leu Gly Phe Leu Gly Phe Leu  
 485 490 495

Ala Thr Ala Gly Ser Ala Met Gly Ala Ala Ser Val Thr Leu Thr Ala  
 500 505 510

Gln Ser Arg Thr Ser Leu Ala Gly Ile Val Gln Gln Gln Gln Gln Leu  
 515 520 525

Leu Asp Val Val Lys Lys Gln Gln Glu Met Leu Arg Leu Thr Val Trp  
 530 535 540

Gly Thr Lys Asn Leu Gln Thr Arg Val Thr Ala Ile Glu Lys Tyr Leu  
 545 550 555 560

Lys Asp Gln Ala Gln Leu Asn Ser Trp Gly Cys Ala Phe Arg Gln Val  
 565 570 575

Cys His Thr Ser Val Pro Trp Val Asn Asp Ser Leu Thr Pro Asp Trp  
 580 585 590

Asn Asn Met Thr Trp Gln Glu Trp Glu Gln Lys Val Arg Tyr Trp Glu  
 595 600 605

Ala Asn Ile Ser Gln Ser Leu Glu Gln Ala Gln Ile Gln Gln Glu Lys  
 610 615 620

Asn Leu Tyr Glu Leu Gln Lys Leu Asn Ser Trp Gly Val Phe Thr Asn  
 625 630 635 640

Trp Leu Asp Phe Thr Ser Trp Val Arg Tyr Ile Gln Tyr Gly Val Tyr  
 645 650 655

Val Val Val Gly Ile Val Thr Leu Arg Ile Val Ile Tyr Ile Val Gln  
 660 665 670

Met Leu Ser Arg Leu Arg Lys Gly Tyr Arg Pro Val Phe Ser Ser Pro  
 675 680 685

Pro Gly Tyr Ile Gln Gln Ile His Ile His Lys Asp Gln Glu Gln Pro

690

695

700

Ala Arg Glu Glu Thr Glu Glu Asp Val Gly Ser Asn Gly Gly Asp Arg  
 705 710 715 720

Ser Trp Leu

<210> 23  
 <211> 485  
 <212> PRT  
 <213> HIV-2/VCP Clone p16.9 (gp120)  
 <400> 23

Met Lys Gly Ser Lys Asn Gln Leu Leu Ile Ala Ile Ile Leu Ala Ser  
 1 5 10 15

Ala Tyr Leu Thr His Cys Lys Gln Phe Val Thr Val Phe Tyr Gly Ile  
 20 25 30

Pro Ala Trp Arg Asn Ala Ser Ile Pro Leu Phe Cys Ala Thr Lys Asn  
 35 40 45

Arg Asp Thr Trp Gly Thr Ile Gln Cys Leu Pro Asp Asn Asp Asp Tyr  
 50 55 60

Gln Glu Ile Ala Leu Asn Val Thr Glu Ala Phe Asp Ala Trp Asn Asn  
 65 70 75 80

Thr Val Thr Glu Gln Ala Val Glu Asp Val Trp Asn Leu Phe Glu Thr  
 85 90 95

Ser Ile Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Ala Met Asn  
 100 105 110

Cys Thr Arg Asn Met Thr Thr Ser Thr Gly Thr Thr Asp Thr Gln Asn  
 115 120 125

Ile Thr Ile Ile Asn Asp Thr Ser Pro Cys Val Arg Ala Asp Asn Cys  
 130 135 140

Thr Gly Leu Lys Glu Glu Glu Met Val Asp Cys Gln Phe Asn Met Thr  
 145 150 155 160

Gly Leu Glu Arg Asp Lys Arg Lys Gln Tyr Thr Gly Ala Trp Tyr Ser  
165 170 175

Lys Asp Val Ile Cys Asp Asn Asn Thr Ser Ser Arg Ser Lys Cys Tyr  
180 185 190

Met Asn His Cys Asn Thr Ser Val Ile Thr Glu Ser Cys Asp Lys His  
195 200 205

Tyr Trp Asp Ala Met Arg Phe Arg Tyr Cys Ala Pro Pro Gly Phe Ala  
210 215 220

Leu Leu Arg Cys Asn Asp Thr Asn Tyr Ser Gly Phe Ala Pro Asn Cys  
225 230 235 240

Ser Lys Val Val Ala Ala Thr Cys Thr Arg Met Met Glu Thr Gln Ser  
245 250 255

Ser Thr Trp Phe Gly Phe Asn Gly Thr Arg Ala Glu Asn Arg Thr Tyr  
260 265 270

Ile Tyr Trp His Gly Lys Asn Asn Arg Thr Ile Ile Ser Leu Asn Asn  
275 280 285

Phe Tyr Asn Leu Thr Met His Cys Lys Arg Pro Gly Asn Lys Gly Ala  
290 295 300

Gly Lys Pro Arg Gln Ala Trp Cys Trp Phe Lys Gly Glu Trp Lys Glu  
305 310 315 320

Ala Met Gln Glu Val Lys Glu Thr Leu Ala Lys His Pro Arg Tyr Lys  
325 330 335

Gly Asn Arg Ser Arg Thr Glu Asn Ile Lys Phe Lys Ala Pro Gly Arg  
340 345 350

Gly Ser Asp Pro Glu Ala Ala Tyr Met Trp Thr Asn Cys Arg Gly Glu  
355 360 365

Phe Leu Tyr Cys Asn Met Ala Trp Phe Leu Asn Trp Val Asp Asn Arg  
370 375 380

Thr Gly Gln Lys Gln Arg Asn Tyr Ala Pro Cys His Ile Arg Gln Ile  
 385 390 395 400

Ile Asn Thr Trp His Arg Val Gly Lys Asn Ile Tyr Leu Pro Pro Arg  
 405 410 415

Glu Gly Glu Leu Thr Cys Asn Ser Thr Val Thr Ser Ile Ile Ala Asn  
 420 425 430

Ile Asp Thr Gly Asp Gln Thr Asp Ile Thr Phe Ser Ala Glu Val Ala  
 435 440 445

Glu Leu Tyr Arg Leu Glu Leu Gly Asp Tyr Lys Leu Val Glu Ile Thr  
 450 455 460

Pro Ile Gly Phe Ala Pro Thr Ser Val Lys Arg Tyr Ser Ser Ala His  
 465 470 475 480

Gln Arg His Thr Arg  
 485

<210> 24  
 <211> 238  
 <212> PRT  
 <213> HIV-2/VCP Clone p16.9 (gp41)  
 <400> 24

Gly Val Phe Val Leu Gly Phe Leu Gly Phe Leu Ala Thr Ala Gly Ser  
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Ala Met Gly Ala Ala Ser Val Thr Leu Thr Ala Gln Ser Arg Thr Ser  
 20 25 30

Leu Ala Gly Ile Val Gln Gln Gln Gln Leu Leu Asp Val Val Lys  
 35 40 45

Lys Gln Gln Glu Met Leu Arg Leu Thr Val Trp Gly Thr Lys Asn Leu  
 50 55 60

Gln Thr Arg Val Thr Ala Ile Glu Lys Tyr Leu Lys Asp Gln Ala Gln  
 65 70 75 80

Leu Asn Ser Trp Gly Cys Ala Phe Arg Gln Val Cys His Thr Ser Val  
 85 90 95

Pro Trp Val Asn Asp Ser Leu Thr Pro Asp Trp Asn Asn Met Thr Trp  
100 105 110

Gln Glu Trp Glu Gln Lys Val Arg Tyr Trp Glu Ala Asn Ile Ser Gln  
115 120 125

Ser Leu Glu Gln Ala Gln Ile Gln Gln Glu Lys Asn Leu Tyr Glu Leu  
130 135 140

Gln Lys Leu Asn Ser Trp Gly Val Phe Thr Asn Trp Leu Asp Phe Thr  
145 150 155 160

Ser Trp Val Arg Tyr Ile Gln Tyr Gly Val Tyr Val Val Val Gly Ile  
165 170 175

Val Thr Leu Arg Ile Val Ile Tyr Ile Val Gln Met Leu Ser Arg Leu  
180 185 190

Arg Lys Gly Tyr Arg Pro Val Phe Ser Ser Pro Pro Gly Tyr Ile Gln  
195 200 205

Gln Ile His Ile His Lys Asp Gln Glu Gln Pro Ala Arg Glu Glu Thr  
210 215 220

Glu Glu Asp Val Gly Ser Asn Gly Gly Asp Arg Ser Trp Leu  
225 230 235

<210> 25  
<211> 2142  
<212> DNA  
<213> HIV-2/VCP Clone 8c.3 (env)

<400> 25  
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cccctgtttt gtgcaaccaa aaatagagat acttggggaa ccatacagtg cttgccagac 180  
aatgatgatt atcaggaaat agctctaaat gtaacagagg ctttcgatgc atggaataat 240  
acagtaacag aacaagcagt ggaggatgtc tggaatctat ttgagacatc aataaaacca 300  
tgtgtcaaat taacaccctt atgtgtagca atgaactgta caaggaacat gaccacatcc 360  
acagggacca cagacacca aaatatcaca attataaatg acatttcgcc atgcgtacgt 420



gcagacaact gcacaggatt aaaggaggaa gaaatggtcg actgtcagtt taatatgaca	480
ggattagaga gagacaagag aaaacagtat actggaacat ggtactcaaa agatgtgatt	540
tgtgacaata acacctcaag tcggagcaag tgttacatga accattgcaa tacatcagtc	600
atcacaaagt catgtgataa gcactattgg gatgctatga ggttttagata ctgtgcacca	660
ccgggttttg ccctactaag atgcaatgat actaattatt caggctttgc acctaattgc	720
tctaaagtag tagctgctac atgcaccaga atgatggaaa cgcaatcttc tacatggttt	780
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agaactatta tcagcttaaa taacttttat aatctcacta tgcattgtaa gggtgccggc	900
tgggtgttgg tcaaaggcga atggaaggaa gccatgcagg aggtgaagga gacccttgcg	960
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tactgcaaca tggcttggtt cctcaactgg gtagataaca ggacgggtcg gaaacagcgc	1140
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gccaacattg atacgggaga tcaaacagat attacctta gtgcagagggt ggcagaacta	1320
taccgattgg aattgggaga ttacaaatta gtagaaatca caccaattgg ctctgcacct	1380
acatcagtaa agagatactc ctctgctcac cagagacata caagagggtgt gttcgtgcta	1440
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accgcccagt cccggacttc attggctggg atagtgcagc aacagcaaca gctgttgagc	1560
gtggtcaaga aacaacaaga aatgttgcca ctgaccgtct ggggaactaa aaatctccag	1620
acaagagtca ctgctataga gaaataccta aaggaccagg cgcagttaaa ttcattgggga	1680
tgtgcgttta gacaagtctg ccacacttct gtaccatggg taaatgatag cttgacacct	1740
gattggaaca atatgacgtg gcaggaatgg gaacagaaag tccgctactg ggaggcaa	1800
atcagtcaaa gtctagaaca agcacaaatt cagcaagaaa agaatttgta tgagctgcaa	1860
aaattaaata gctgggggtgt ttttaccat tggcttgact tcacctctg ggtcaggtat	1920
attcaatatg gagcatatgt agtagtagga atagtaactt taagaatagt aatatatata	1980
gtacagatgt taagtagact taggaagggc tataggcctg ttttctcctc ccccccggt	2040
tatatccaac agatccatat ccacaaggac caggaacagc cagccagaga agaaacagaa	2100

gaagacgttg gaagcaacgg tggagacaga tcttggcttt ag 2142

<210> 26

<211> 1425

<212> DNA

<213> HIV-2/VCP Clone 8c.3 (gp120)

<400> 26

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cccctgtttt gtgcaaccaa aaatagagat acttggggaa ccatacagtg cttgccagac 180  
aatgatgatt atcaggaaat agctctaaat gtaacagagg ctttcgatgc atggaataat 240  
acagtaacag aacaagcagt ggaggatgtc tggaatctat ttgagacatc aataaaacca 300  
tgtgtcaaat taacaccctt atgtgtagca atgaactgta caaggaacat gaccacatcc 360  
acagggacca cagacacca aaatatcaca attataaatg acacttcgcc atgcgtacgt 420  
gcagacaact gcacaggatt aaaggaggaa gaaatggtcg actgtcagtt taatatgaca 480  
ggattagaga gagacaagag aaaacagtat actggaacat ggtactcaaa agatgtgatt 540  
tgtgacaata acacctcaag tcggagcaag tgttacatga accattgcaa tacatcagtc 600  
atcacaaagt catgtgataa gcactattgg gatgctatga ggtttagata ctgtgcacca 660  
ccgggttttg ccctactaag atgcaatgat actaattatt caggctttgc acctaattgc 720  
tctaaagtag tagctgctac atgcaccaga atgatggaaa cgcaatcttc tacatggttt 780  
ggatttaatg gcactagagc agaaaataga acatatatat attggcatgg taaaaataac 840  
agaactatta tcagcttaaa taacttttat aatctcacta tgcattgtaa gggtgccggc 900  
tggtgttggt tcaaaggcga atggaaggaa gccatgcagg aggtgaagga gacccttgcg 960  
aaacatccca gatataaagg gaacaggagc cgcacagaga atattaaatt taaagcacca 1020  
ggaagaggct cagaccaga agcagcatac atgtggacta actgcagagg ggaatttctc 1080  
tactgcaaca tggcttggtt cctcaactgg gtagataaca ggacgggtcg gaaacagcgc 1140  
aattatgcac cgtgccatat aaggcaaata attaatactt ggcacagggt agggaaaaac 1200  
atatatttgc ctcccaggga aggggagttg gcctgcaact caacagtgc cagcataatt 1260  
gccaacattg atacgggaga tcaaacagat attaccttta gtgcagaggt ggcagaacta 1320  
taccgattgg aattgggaga ttacaaatta gtagaaatca caccaattgg cttcgcacct 1380  
acatcagtaa agagatactc ctctgctcac cagagacata caaga 1425

<210> 27  
 <211> 717  
 <212> DNA  
 <213> HIV-2/VCP Clone 8c.3 (gp41)

<400> 27  
 ggtgtgttcg tgctaggggtt cttggggtttt ctcgcaacgg cagggttctgc aatggg'gcgcg 60  
 gcgtcgggtga cgctgaccgc ccagtcccgg acttcattgg ctgggatagt gcagcaacag 120  
 caacagctgt tggacgtggt caagaaacaa caagaaatgt tgcgactgac cgtctgggga 180  
 actaaaaatc tccagacaag agtcactgct atagagaaat acctaaagga ccaggcgcag 240  
 ttaaattcat ggggatgtgc gtttagacaa gtctgccaca cttctgtacc atgggtaaat 300  
 gatagcttga cacctgattg gaacaatatg acgtggcagg aatgggaaca gaaagtccgc 360  
 tactgggagg caaatatcag tcaaagtcta gaacaagcac aaattcagca agaaaagaat 420  
 ttgtatgagc tgcaaaaatt aaatagctgg ggtgttttta ccaattggct tgacttcacc 480  
 tcctgggtca ggtatattca atatggagca tatgtagtag taggaatagt aactttaaga 540  
 atagtaatat atatagtaca gatgttaagt agacttagga agggctatag gcctgttttc 600  
 tcctcccccc ccggttatat ccaacagatc catatccaca aggaccagga acagccagcc 660  
 agagaagaaa cagaagaaga cgttggaagc aacggtggag acagatcttg gcttttag 717

<210> 28  
 <211> 713  
 <212> PRT  
 <213> HIV-2/VCP Clone 8c.3 (env)

<400> 28

Met Lys Gly Ser Lys Asn Gln Leu Leu Ile Ala Ile Ile Leu Ala Ser  
 1 5 10 15

Ala Tyr Leu Thr His Cys Lys Gln Phe Val Thr Val Phe Tyr Gly Ile  
 20 25 30

Pro Ala Trp Arg Asn Ala Ser Ile Pro Leu Phe Cys Ala Thr Lys Asn  
 35 40 45

Arg Asp Thr Trp Gly Thr Ile Gln Cys Leu Pro Asp Asn Asp Asp Tyr  
 50 55 60

Gln Glu Ile Ala Leu Asn Val Thr Glu Ala Phe Asp Ala Trp Asn Asn  
 65 70 75 80

Thr Val Thr Glu Gln Ala Val Glu Asp Val Trp Asn Leu Phe Glu Thr  
85 90 95

Ser Ile Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Ala Met Asn  
100 105 110

Cys Thr Arg Asn Met Thr Thr Ser Thr Gly Thr Thr Asp Thr Gln Asn  
115 120 125

Ile Thr Ile Ile Asn Asp Thr Ser Pro Cys Val Arg Ala Asp Asn Cys  
130 135 140

Thr Gly Leu Lys Glu Glu Glu Met Val Asp Cys Gln Phe Asn Met Thr  
145 150 155 160

Gly Leu Glu Arg Asp Lys Arg Lys Gln Tyr Thr Gly Thr Trp Tyr Ser  
165 170 175

Lys Asp Val Ile Cys Asp Asn Asn Thr Ser Ser Arg Ser Lys Cys Tyr  
180 185 190

Met Asn His Cys Asn Thr Ser Val Ile Thr Lys Ser Cys Asp Lys His  
195 200 205

Tyr Trp Asp Ala Met Arg Phe Arg Tyr Cys Ala Pro Pro Gly Phe Ala  
210 215 220

Leu Leu Arg Cys Asn Asp Thr Asn Tyr Ser Gly Phe Ala Pro Asn Cys  
225 230 235 240

Ser Lys Val Val Ala Ala Thr Cys Thr Arg Met Met Glu Thr Gln Ser  
245 250 255

Ser Thr Trp Phe Gly Phe Asn Gly Thr Arg Ala Glu Asn Arg Thr Tyr  
260 265 270

Ile Tyr Trp His Gly Lys Asn Asn Arg Thr Ile Ile Ser Leu Asn Asn  
275 280 285

Phe Tyr Asn Leu Thr Met His Cys Lys Gly Ala Gly Trp Cys Trp Phe  
290 295 300

Lys Gly Glu Trp Lys Glu Ala Met Gln Glu Val Lys Glu Thr Leu Ala  
 305 310 315 320

Lys His Pro Arg Tyr Lys Gly Asn Arg Ser Arg Thr Glu Asn Ile Lys  
 325 330 335

Phe Lys Ala Pro Gly Arg Gly Ser Asp Pro Glu Ala Ala Tyr Met Trp  
 340 345 350

Thr Asn Cys Arg Gly Glu Phe Leu Tyr Cys Asn Met Ala Trp Phe Leu  
 355 360 365

Asn Trp Val Asp Asn Arg Thr Gly Arg Lys Gln Arg Asn Tyr Ala Pro  
 370 375 380

Cys His Ile Arg Gln Ile Ile Asn Thr Trp His Arg Val Gly Lys Asn  
 385 390 395 400

Ile Tyr Leu Pro Pro Arg Glu Gly Glu Leu Ala Cys Asn Ser Thr Val  
 405 410 415

Thr Ser Ile Ile Ala Asn Ile Asp Thr Gly Asp Gln Thr Asp Ile Thr  
 420 425 430

Phe Ser Ala Glu Val Ala Glu Leu Tyr Arg Leu Glu Leu Gly Asp Tyr  
 435 440 445

Lys Leu Val Glu Ile Thr Pro Ile Gly Phe Ala Pro Thr Ser Val Lys  
 450 455 460

Arg Tyr Ser Ser Ala His Gln Arg His Thr Arg Gly Val Phe Val Leu  
 465 470 475 480

Gly Phe Leu Gly Phe Leu Ala Thr Ala Gly Ser Ala Met Gly Ala Ala  
 485 490 495

Ser Val Thr Leu Thr Ala Gln Ser Arg Thr Ser Leu Ala Gly Ile Val  
 500 505 510

Gln Gln Gln Gln Gln Leu Leu Asp Val Val Lys Lys Gln Gln Glu Met  
 515 520 525

Leu Arg Leu Thr Val Trp Gly Thr Lys Asn Leu Gln Thr Arg Val Thr  
 530 535 540

Ala Ile Glu Lys Tyr Leu Lys Asp Gln Ala Gln Leu Asn Ser Trp Gly  
 545 550 555 560

Cys Ala Phe Arg Gln Val Cys His Thr Ser Val Pro Trp Val Asn Asp  
 565 570 575

Ser Leu Thr Pro Asp Trp Asn Asn Met Thr Trp Gln Glu Trp Glu Gln  
 580 585 590

Lys Val Arg Tyr Trp Glu Ala Asn Ile Ser Gln Ser Leu Glu Gln Ala  
 595 600 605

Gln Ile Gln Gln Glu Lys Asn Leu Tyr Glu Leu Gln Lys Leu Asn Ser  
 610 615 620

Trp Gly Val Phe Thr Asn Trp Leu Asp Phe Thr Ser Trp Val Arg Tyr  
 625 630 635 640

Ile Gln Tyr Gly Ala Tyr Val Val Val Gly Ile Val Thr Leu Arg Ile  
 645 650 655

Val Ile Tyr Ile Val Gln Met Leu Ser Arg Leu Arg Lys Gly Tyr Arg  
 660 665 670

Pro Val Phe Ser Ser Pro Pro Gly Tyr Ile Gln Gln Ile His Ile His  
 675 680 685

Lys Asp Gln Glu Gln Pro Ala Arg Glu Glu Thr Glu Glu Asp Val Gly  
 690 695 700

Ser Asn Gly Gly Asp Arg Ser Trp Leu  
 705 710

<210> 29  
 <211> 475  
 <212> PRT  
 <213> HIV-2/VCP Clone 8c.3 (gp120)

<400> 29

Met Lys Gly Ser Lys Asn Gln Leu Leu Ile Ala Ile Ile Leu Ala Ser  
 1 5 10 15

Ala Tyr Leu Thr His Cys Lys Gln Phe Val Thr Val Phe Tyr Gly Ile  
20 25 30

Pro Ala Trp Arg Asn Ala Ser Ile Pro Leu Phe Cys Ala Thr Lys Asn  
35 40 45

Arg Asp Thr Trp Gly Thr Ile Gln Cys Leu Pro Asp Asn Asp Asp Tyr  
50 55 60

Gln Glu Ile Ala Leu Asn Val Thr Glu Ala Phe Asp Ala Trp Asn Asn  
65 70 75 80

Thr Val Thr Glu Gln Ala Val Glu Asp Val Trp Asn Leu Phe Glu Thr  
85 90 95

Ser Ile Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Ala Met Asn  
100 105 110

Cys Thr Arg Asn Met Thr Thr Ser Thr Gly Thr Thr Asp Thr Gln Asn  
115 120 125

Ile Thr Ile Ile Asn Asp Thr Ser Pro Cys Val Arg Ala Asp Asn Cys  
130 135 140

Thr Gly Leu Lys Glu Glu Glu Met Val Asp Cys Gln Phe Asn Met Thr  
145 150 155 160

Gly Leu Glu Arg Asp Lys Arg Lys Gln Tyr Thr Gly Thr Trp Tyr Ser  
165 170 175

Lys Asp Val Ile Cys Asp Asn Asn Thr Ser Ser Arg Ser Lys Cys Tyr  
180 185 190

Met Asn His Cys Asn Thr Ser Val Ile Thr Lys Ser Cys Asp Lys His  
195 200 205

Tyr Trp Asp Ala Met Arg Phe Arg Tyr Cys Ala Pro Pro Gly Phe Ala  
210 215 220

Leu Leu Arg Cys Asn Asp Thr Asn Tyr Ser Gly Phe Ala Pro Asn Cys  
225 230 235 240

Ser Lys Val Val Ala Ala Thr Cys Thr Arg Met Met Glu Thr Gln Ser  
 245 250 255

Ser Thr Trp Phe Gly Phe Asn Gly Thr Arg Ala Glu Asn Arg Thr Tyr  
 260 265 270

Ile Tyr Trp His Gly Lys Asn Asn Arg Thr Ile Ile Ser Leu Asn Asn  
 275 280 285

Phe Tyr Asn Leu Thr Met His Cys Lys Gly Ala Gly Trp Cys Trp Phe  
 290 295 300

Lys Gly Glu Trp Lys Glu Ala Met Gln Glu Val Lys Glu Thr Leu Ala  
 305 310 315 320

Lys His Pro Arg Tyr Lys Gly Asn Arg Ser Arg Thr Glu Asn Ile Lys  
 325 330 335

Phe Lys Ala Pro Gly Arg Gly Ser Asp Pro Glu Ala Ala Tyr Met Trp  
 340 345 350

Thr Asn Cys Arg Gly Glu Phe Leu Tyr Cys Asn Met Ala Trp Phe Leu  
 355 360 365

Asn Trp Val Asp Asn Arg Thr Gly Arg Lys Gln Arg Asn Tyr Ala Pro  
 370 375 380

Cys His Ile Arg Gln Ile Ile Asn Thr Trp His Arg Val Gly Lys Asn  
 385 390 395 400

Ile Tyr Leu Pro Pro Arg Glu Gly Glu Leu Ala Cys Asn Ser Thr Val  
 405 410 415

Thr Ser Ile Ile Ala Asn Ile Asp Thr Gly Asp Gln Thr Asp Ile Thr  
 420 425 430

Phe Ser Ala Glu Val Ala Glu Leu Tyr Arg Leu Glu Leu Gly Asp Tyr  
 435 440 445

Lys Leu Val Glu Ile Thr Pro Ile Gly Phe Ala Pro Thr Ser Val Lys  
 450 455 460



Arg Tyr Ser Ser Ala His Gln Arg His Thr Arg  
 465 470 475

<210> 30  
 <211> 238  
 <212> PRT  
 <213> HIV-2/VCP Clone 8c.3 (gp41)

<400> 30

Gly Val Phe Val Leu Gly Phe Leu Gly Phe Leu Ala Thr Ala Gly Ser  
 1 5 10 15

Ala Met Gly Ala Ala Ser Val Thr Leu Thr Ala Gln Ser Arg Thr Ser  
 20 25 30

Leu Ala Gly Ile Val Gln Gln Gln Gln Gln Leu Leu Asp Val Val Lys  
 35 40 45

Lys Gln Gln Glu Met Leu Arg Leu Thr Val Trp Gly Thr Lys Asn Leu  
 50 55 60

Gln Thr Arg Val Thr Ala Ile Glu Lys Tyr Leu Lys Asp Gln Ala Gln  
 65 70 75 80

Leu Asn Ser Trp Gly Cys Ala Phe Arg Gln Val Cys His Thr Ser Val  
 85 90 95

Pro Trp Val Asn Asp Ser Leu Thr Pro Asp Trp Asn Asn Met Thr Trp  
 100 105 110

Gln Glu Trp Glu Gln Lys Val Arg Tyr Trp Glu Ala Asn Ile Ser Gln  
 115 120 125

Ser Leu Glu Gln Ala Gln Ile Gln Gln Glu Lys Asn Leu Tyr Glu Leu  
 130 135 140

Gln Lys Leu Asn Ser Trp Gly Val Phe Thr Asn Trp Leu Asp Phe Thr  
 145 150 155 160

Ser Trp Val Arg Tyr Ile Gln Tyr Gly Ala Tyr Val Val Val Gly Ile  
 165 170 175

Val Thr Leu Arg Ile Val Ile Tyr Ile Val Gln Met Leu Ser Arg Leu  
 180 185 190

Arg Lys Gly Tyr Arg Pro Val Phe Ser Ser Pro Pro Gly Tyr Ile Gln  
195 200 205

Gln Ile His Ile His Lys Asp Gln Glu Gln Pro Ala Arg Glu Glu Thr  
210 215 220

Glu Glu Asp Val Gly Ser Asn Gly Gly Asp Arg Ser Trp Leu  
225 230 235